SEQUENCE LISTING

<110> xantos biomedicine AG

<120> A new angiogenic factor and its medical use

<130> X62815PC

<150> US 60/477,470

<151> 2003-06-10

<150> US 60/503,388

<151> 2003-09-16

<160> 31

<170> PatentIn version 3.1

<210> 1

<211> 3020

<212> DNA

<213> Mus musculus

<400> 1

ctcaggactc tgtgttcact gagatccttc agggagggaa ccttggctag ggccagttac 60

gcctgggagt ccgcatgggc gccctgggcc tgggcgcgtg gggtcggaga ggctcctgaa 120

ctaggggaga atgaggtcgg ccacacacgg attcgcgacc ccggcagttc cttgatccgc 180

atccagcacc tttagcaagc agtccatctc agtccatccc accctgccag ggtccgagtc 240

actccagaag ctgagcagcc atgacatttg ctgaggacaa gacctataag tatatccgag 300

acaaccacag caagttttgc tgtgttgacg ttctggagat cctgccttac ctgtcctgcc 360

tcacagctag tgaccaggat cgactgcggg cttcctacag gcagatcggg aaccgggaca 420

cactctgggg actcttcaat aatctccagc gccggcctgg ctgggtggag gtcttcatcc 480

gggcactgca gatctgtgag ctgcctgggc tggctgatca agtgactcga gtttatcaga 540

gctacctgcc tccggggacc tcactccgct ccctagagcc actgcagtta ccagactttc 600

ctgctgcggt ttctggaccc tctgcatttg cgccaggtca caacatccct gaccatggct 660

tacgagagac accaagttgc cccaagcctg tccaggacac ccagccacca gagtccccag 720

tagagaattc agagcaactc ctccagacca actccggggc cgtcgcgagg atgtctggtg 780

gctctttgat accctctcct aaccagcagg ctctcagccc tcagccctcc agagagcatc 840

aagagcaaga accagaactg ggtggcgccc acgcagcaaa tgttgcctct gttcccatag 900

caacctatgg acctgtgtct ccaaccgttt ccttccagcc ccttccacgt actgccctga 960

ggacaaacct cttgtctggg gtcacagtat cagccctatc tgctgatacc tctttgtcct 1020

cctcgtccac tggatcagct tttgcaaagg gagctggtga ccaggccaaa gctgccacct 1080

gtttcagtac tacactcacc aattctgtga ctaccagctc agtgccttct cccagattgg 1140

tcccagtaaa aaccatgtct tccaagttgc ccctcagttc aaagtccact gctgcgatga 1200

cgtctactgt gctcaccaat acagcgccat caaaattacc cagcaactca gtgtatgcgg 1260

gcacagtgcc atccagagtg cctgctagtg tggccaaagc acctgccaac acaataccac 1320

ctgagaggaa cagcaagcaa gccaaggaga ccccggaggg tccagcaacc aaagtcacca 1380

ctggaggcaa ccagactgga ccaaatagca gtatcaggag cttgcactct ggaccagaga 1440

tgagcaagcc aggtgtgctg gtatcccagt tggacgagcc attctcagcc tgctctgtgg 1500

accttgccat tagccctagc agctccttgg tctcagaacc caaccatggt ccagaggaga 1560

atgagtattc gtcctttaga atccaggtag acgaaagccc cagtgctgat ctattaggaa 1620

gccctgagcc actagccacc cagcagcccc aagaagagga agaacattgt gccagttcaa 1680

tgccctgggc taagtggctt ggggccacca gtgcactctt ggctgtattc ctggcagtga 1740

tgctgtaccg tagtaggcgc ctggcccagt gaagcctcag ctgtatgctg ttctcttgct 1800

cagttctgcc aagcatgttc tctaggcttg ggctagtaga ggctgagtca gagaaactta 1860

aatatggcga ggtccactga gctatccagg tagatagcta caccaagacg tcatcactgt 1920

tgggtggggg agagacattg ttttatcctg gttcatatgt catcttctgg tcttcagctt 1980

ttggaggcac tgtgttacct ccattgctcc tgacctgccc acgtggcagt gtaagagttc 2040

atgctctgtg ctcctaagga ggtatctcca ccagctttat ccctgttggc ccaagcctga 2100

agatgaggag gtatcgcact gttgacaatg cccctcatct cgcccagatc ttctgaaaca 2160

caagcgtagg tacactgatg agtgctccca tagcatctta tgccttccac cggcagcctg 2220

gtctaaggcc ttggcaggag agcctgggag taacagagtg gctggtctct agggagcttt 2280

gagtgctctg ccccttgggg ccctctccac agccagtcaa ccctgagggt gagtctggag 2340

gttctctgtg gactcttaag aaagccagaa gcaactgcca ggcctgagga agcccctggg 2400

agggagcttt tctccaacct ccttaccccc tcctcgcttc tccactcctg gtctccattc 2460

tctccctata ctggatgatg agatacctag tgggcagaac tcaggctggg cttgcatcag 2520

ttccaccctt tccctggcct ttagcagatg tctagcttct ctagtcttgt tcccaatgta 2580

gatagcgggc agctcttcct tttactgggc tcctctgagt ttgaaggata cagatacttg 2640

cctagtactt atctcagagg gtgtgagtac aagttcttgc cctcctgccc tggctggctg 2700

agctaaggtg agagtgtgag aggcagagtg catattggta atggcagtct ttgagagagc 2760

agccttcatc tccatcatgc ttctttctcc tccctggtca ggtgtaggcc tcacctctgt 2820

gcctcacttt tcttacctgt gagatggggt gagtatgtgt gtgtatacac acacataccc 2880

acagacccac gcccacaccc acacatacat gctaatatat tctcacctgt gagatggaaa 2940

gtatgcatac attgatgcta atatattcta gttttatcag gataattaaa agagtttatc 3000

tgtgcaaaaa aaaaaaaaaa 3020

<210> 2

<211> 503

<212> PRT

<213> Mus musculus

<400> 2

Met Thr Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Arg Asp Asn His
1 5 10 15

Ser Lys Phe Cys Cys Val Asp Val Leu Glu Ile Leu Pro Tyr Leu Ser
20 25 30

Cys Leu Thr Ala Ser Asp Gln Asp Arg Leu Arg Ala Ser Tyr Arg Gln
35 40 45

Ile Gly Asn Arg Asp Thr Leu Trp Gly Leu Phe Asn Asn Leu Gln Arg
50 55 60

Arg Pro Gly Trp Val Glu Val Phe Ile Arg Ala Leu Gln Ile Cys Glu
65 70 75 80

Leu Pro Gly Leu Ala Asp Gln Val Thr Arg Val Tyr Gln Ser Tyr Leu
85 90 95

Pro Pro Gly Thr Ser Leu Arg Ser Leu Glu Pro Leu Gln Leu Pro Asp
100 105 110

```
Phe Pro Ala Ala Val Ser Gly Pro Ser Ala Phe Ala Pro Gly His Asn
        115                 120                 125

Ile Pro Asp His Gly Leu Arg Glu Thr Pro Ser Cys Pro Lys Pro Val
    130                 135                 140

Gln Asp Thr Gln Pro Pro Glu Ser Pro Val Glu Asn Ser Glu Gln Leu
145                 150                 155                 160

Leu Gln Thr Asn Ser Gly Ala Val Ala Arg Met Ser Gly Gly Ser Leu
                165                 170                 175

Ile Pro Ser Pro Asn Gln Gln Ala Leu Ser Pro Gln Pro Ser Arg Glu
            180                 185                 190

His Gln Glu Gln Glu Pro Glu Leu Gly Gly Ala His Ala Ala Asn Val
        195                 200                 205

Ala Ser Val Pro Ile Ala Thr Tyr Gly Pro Val Ser Pro Thr Val Ser
    210                 215                 220

Phe Gln Pro Leu Pro Arg Thr Ala Leu Arg Thr Asn Leu Leu Ser Gly
225                 230                 235                 240

Val Thr Val Ser Ala Leu Ser Ala Asp Thr Ser Leu Ser Ser Ser Ser
                245                 250                 255

Thr Gly Ser Ala Phe Ala Lys Gly Ala Gly Asp Gln Ala Lys Ala Ala
            260                 265                 270

Thr Cys Phe Ser Thr Thr Leu Thr Asn Ser Val Thr Thr Ser Ser Val
        275                 280                 285

Pro Ser Pro Arg Leu Val Pro Val Lys Thr Met Ser Ser Lys Leu Pro
    290                 295                 300

Leu Ser Ser Lys Ser Thr Ala Ala Met Thr Ser Thr Val Leu Thr Asn
305                 310                 315                 320

Thr Ala Pro Ser Lys Leu Pro Ser Asn Ser Val Tyr Ala Gly Thr Val
                325                 330                 335

Pro Ser Arg Val Pro Ala Ser Val Ala Lys Ala Pro Ala Asn Thr Ile
            340                 345                 350

Pro Pro Glu Arg Asn Ser Lys Gln Ala Lys Glu Thr Pro Glu Gly Pro
        355                 360                 365
```

Ala Thr Lys Val Thr Thr Gly Gly Asn Gln Thr Gly Pro Asn Ser Ser
370 375 380

Ile Arg Ser Leu His Ser Gly Pro Glu Met Ser Lys Pro Gly Val Leu
385 390 395 400

Val Ser Gln Leu Asp Glu Pro Phe Ser Ala Cys Ser Val Asp Leu Ala
405 410 415

Ile Ser Pro Ser Ser Ser Leu Val Ser Glu Pro Asn His Gly Pro Glu
420 425 430

Glu Asn Glu Tyr Ser Ser Phe Arg Ile Gln Val Asp Glu Ser Pro Ser
435 440 445

Ala Asp Leu Leu Gly Ser Pro Glu Pro Leu Ala Thr Gln Gln Pro Gln
450 455 460

Glu Glu Glu Glu His Cys Ala Ser Ser Met Pro Trp Ala Lys Trp Leu
465 470 475 480

Gly Ala Thr Ser Ala Leu Leu Ala Val Phe Leu Ala Val Met Leu Tyr
485 490 495

Arg Ser Arg Arg Leu Ala Gln
500

<210> 3

<211> 2967

<212> DNA

<213> Homo sapiens

<400> 3

ggcggcggtc gccaggtctc agggccgggg gtacccgagt ctcgtttcct ctcagtccat 60

ccaccccttca tggggccaga gccctctctc cagaatctga gcagcaatgc cgtttgctga 120

agacaagacc tataagtata tctgccgcaa tttcagcaat ttttgcaatg tggatgttgt 180

agagattctg ccttacctgc cctgcctcac agcaagagac caggatcgac tgcgggccac 240

ctgcacactc tcagggaacc gggacaccct ctggcatctc ttcaataccc ttcagcggcg 300

gcccggctgg gtggagtact tcattgcggc actgaggggc tgtgagctag ttgatctcgc 360

ggacgaagtg gcctctgtct acgagagcta ccagcctcgg acctcggacc gtcccccaga 420

cccactggag ccaccgtcac ttcctgctga gaggccaggg ccccccacac ctgctgcggc 480

ccacagcatc ccctacaaca gctgcagaga gaaggagcca agttacccca tgcctgtcca 540

ggagacccag gcgccagagt ccccaggaga gaattcagag caagccctgc agacgctcag 600

ccccagagcc atcccaagga atccagatgg tggccccctg gagtcctcct ctgacctggc 660

agccctcagc cctctgacct ccagcgggca tcaggagaag gacacagaac tgggcagtac 720

ccacacagca ggtgcgacct ccagcctcac accatcccgt gggcctgtgt ctccatctgt 780

ctccttccag cccctggccc gttccacccc cagggcaagc cgcttgcctg gacccacagg 840

gtcagttgta tctactggca cctccttctc ctcctcatcc cctggcttgg cctctgcagg 900

ggctgcagag ggtaaacagg gtgcagagag tgaccaggcc gagcctatca tctgctccag 960

tggggcagag gcacctgcca actctctgcc ctccaaagtg cctaccacct tgatgcctgt 1020

gaacacagtg gccctgaaag tgcctgccaa cccagcatct gtcagcacag tgccctccaa 1080

gttgccaact agctcaaagc cccctggtgc agtgccttct aatgcgctca ccaatccagc 1140

accatccaaa ttgcccatca actcaacccg tgctggcatg gtgccatcca aagtgcctac 1200

tagcatggtg ctcaccaagg tgtctgccag cacagtcccc actgacggga gcagcagaaa 1260

tgaggagacc ccagcagctc caacacccgc cggcgccact ggaggcagct cagcctggct 1320

agacagcagc tttgagaata ggggccttgg gtcggagctg agtaagcctg gcgtgctggc 1380

atcccaggta gacagcccgt tctcgggctg cttcgaggat cttgccatca gtgccagcac 1440

ctccttgggc atggggccct gccatggccc agaggagaat gagtataagt ccgagggcac 1500

ctttgggatc cacgtggctg agaaccccag catccagctc ctggagggca accctgggcc 1560

acctgcggac ccggatggcg gccccaggcc acaagccgac cggaagttcc aggagaggga 1620

ggtgccatgc cacaggccct cacctggggc tctgtggctc caggtggctg tgacaggggt 1680

gctggtagtc acactcctgg tggtgctgta ccggcggcgt ctgcactagt gaagccctgg 1740

gctcttccca ccacccatct gttccgttcc tgcagtacac ctggcccctc tccgaagccc 1800

cttgtccctt tcttggggat tgtggaggct gggtcagagg ggagttaagg gactgcaggc 1860

ctggcagcag gacatgcctt ggctgaacca agtcctgaga gcagcatctc tgtccccacg 1920

gtgccttgtg tgggtccccg tccttggctt tctgggtcct gggctgcccc cagtgctcca 1980

gaccttcccc actggcaatc caggttatca tccatgtcct ccagaggagc ttcctcctcc 2040

aggcctcagc cctgttggcc caggtggagc aggagggacc actggaacat gtggtgcttg 2100

ggaatgcctc tcctgttgca ttggtccctg aaggcctcag ggcaggtatg tggtgtgtgg 2160

gcgactccac aagacctgcc tcccatcctg gcagcccagc ctgagaccgt tgcattgagg 2220

caggcaggag cggcagggtg gctgctctcc aggagcccac ctgccttgag ttcctgcccc 2280

actgggcccc ctcccctgct gggcaatcct gggaaggtct ggaggttcct gtggacctca 2340

gggaagccag gggcagctgt caggcctgag gaagacctgt ggagctcctc tccagcctcc 2400

tctttccctc ccctctggtc tccattctct tcagctccct acatgggctg gggaggagac 2460

acctggtggg cagagctcag gcagaggttt ggatttcagc tccctcactt ccggggctgt 2520

gtggctttgg cagatgtcag acttctggtc ttgcttctcc acgtggacag tgagtatctg 2580

gctcattctt cactgggttc ttctgagatt gaacctacag gtgtttgcca agtgcctggc 2640

ccagagcaag tggccactgc ttctcccatc tctctcctgc ccaacctggt agagctgagg 2700

gcatgagagg cagagtgcac agtggtcaag ggtgcagctc tgcagcacag gcagcctagg 2760

cctgcgtccc aacctgcctc tcaccagctc tgtgaccttg ggcaagggat ttatctgtct 2820

gtcccttagt tttctcacct gtaaaaggag gataagtata tatatatatt tccccagtgt 2880

tgtgaagatt aaagttgttt atcgatgtaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2940

aaaaaaaaaa aaaaaaaaaa aaaaaaa 2967

<210> 4

<211> 540

<212> PRT

<213> Homo sapiens

<400> 4

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe
1 5 10 15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
20 25 30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
35 40 45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
50 55 60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu
65 70 75 80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Glu Ser Tyr Gln
85 90 95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu
100 105 110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
115 120 125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
130 135 140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145 150 155 160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly
165 170 175

Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser
180 185 190

Ser Gly His Gln Glu Lys Asp Thr Glu Leu Gly Ser Thr His Thr Ala
195 200 205

Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser
210 215 220

Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu
225 230 235 240

Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser
245 250 255

Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly
260 265 270

Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu
275 280 285

Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro
290 295 300

Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser
305 310 315 320

Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val
325 330 335

Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn
340 345 350

Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val
355 360 365

Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg
370 375 380

Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly
385 390 395 400

Ser Ser Ala Trp Leu Asp Ser Ser Phe Glu Asn Arg Gly Leu Gly Ser
405 410 415

Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe
420 425 430

Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly
435 440 445

Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly
450 455 460

Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu
465 470 475 480

Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln
485 490 495

Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser
500 505 510

Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val
515 520 525

Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
530 535 540

<210> 5

<211> 4237

<212> DNA

<213> Homo sapiens

<400> 5

gcgggaaggg tcctgggccc cgggcggcgg tcgccaggtc tcagggccgg gggtacccga 60

gtctcgtttc ctctcagtcc atccaccctt catggggcca gagccctctc tccagaatct 120

gagcagcaat gccgtttgct gaagacaaga cctataagta tatctgccgc aatttcagca 180

atttttgcaa tgtggatgtt gtagagattc tgccttacct gccctgcctc acagcaagag 240

accaggatcg actgcgggcc acctgcacac tctcagggaa ccgggacacc ctctggcatc 300

tcttcaatac ccttcagcgg cggcccggct gggtggagta cttcattgcg gcactgaggg 360

gctgtgagct agttgatctc gcggacgaag tggcctctgt ctaccagagc taccagcctc 420

ggacctcgga ccgtccccca gacccactgg agccaccgtc acttcctgct gagaggccag 480

ggccccccac acctgctgcg gcccacagca tcccctacaa cagctgcaga gagaaggagc 540

caagttaccc catgcctgtc caggagaccc aggcgccaga gtccccagga gagaattcag 600

agcaagccct gcagacgctc agccccagag ccatcccaag gaatccagat ggtggccccc 660

tggagtcctc ctctgacctg gcagccctca gccctctgac ctccagcggg catcaggagc 720

aggacacaga actgggcagt acccacacag caggtgcgac ctccagcctc acaccatccc 780

gtgggcctgt gtctccatct gtctccttcc agcccctggc ccgttccacc cccagggcaa 840

gccgcttgcc tggacccaca gggtcagttg tatctactgg cacctccttc tcctcctcat 900

cccctggctt ggcctctgca ggggctgcag agggtaaaca gggtgcagag agtgaccagg 960

ccgagcctat catctgctcc agtggggcag aggcacctgc caactctctg ccctccaaag 1020

tgcctaccac cttgatgcct gtgaacacag tggccctgaa agtgcctgcc aacccagcat 1080

ctgtcagcac agtgccctcc aagttgccaa ctagctcaaa gccccctggt gcagtgcctt 1140

ctaatgcgct caccaatcca gcaccatcca aattgcccat caactcaacc cgtgctggca 1200

tggtgccatc caaagtgcct actagcatgg tgctcaccaa ggtgtctgcc agcacagtcc 1260

ccactgacgg gagcagcaga aatgaggaga ccccagcagc tccaacaccc gccggcgcca 1320

ctggaggcag ctcagcctgg ctagacagca gctctgagaa taggggcctt gggtcggagc 1380

tgagtaagcc tggcgtgctg gcatcccagg tagacagccc gttctcgggc tgcttcgagg 1440

atcttgccat cagtgccagc acctccttgg gcatggggcc ctgccatggc ccagaggaga 1500

atgagtataa gtccgagggc acctttggga tccacgtggc tgagaacccc agcatccagc 1560

tcctggaggg caaccctggg ccacctgcgg acccggatgg cggccccagg ccacaagccg 1620

accggaagtt ccaggagagg gaggtgccat gccacaggcc ctcacctggg gctctgtggc 1680

tccaggtggc tgtgacaggg gtgctggtag tcacactcct ggtggtgctg taccggcggc 1740

gtctgcacta gtgaagccct gggctcttcc caccacccat ctgttccgtt cctgcagtac 1800

acctggcccc tctccgaagc cccttgtccc tttcttgggg attgtggagg ctgggtcaga 1860

ggggagttaa gggactgcag gcctggcagc aggacatgcc ttggctgaac caagtcctga 1920

gagcagcatc tctgtcccca cggtgccttg tgtgggtccc cgtccttggc tttctgggtc 1980

ctgggctgcc cccagtgctc cagaccttcc ccactggcaa tccaggttat catccatgtc 2040

ctccagagga gcttcctcct ccaggcctca gccctgttgg cccaggtgga gcaggaggga 2100

ccactggaac atgtggtgct tgggaatgcc tctcctgttg cattggtccc tgaaggcctc 2160

agggcaggta tgtggtgtgt gggcgactcc acaagacctg cctcccatcc tggcagccca 2220

gcctgagacc gttgcattga ggcaggcagg agcggcaggg tggctgctct ccaggagccc 2280

aactgccttg agttcctgcc ccactgggcc ccctcccctg ctgggcaatc ctgggaaggt 2340

ctggaggttc ctgtggacct cagggaagcc aggggcagct gtcaggcctg aggaagacct 2400

gtggagctcc tctccagcct cctctttccc tcccctctgg tctccattct cttcagctcc 2460

ctacatgggc tggggaggag acacctggtg ggcagagctc aggcagaggt ttggatttca 2520

gctccctcac ttccggggct gtgtggcttt ggcagatgtc agacttctgg tcttgcttct 2580

ccacgtggac agtgagtatc tggctcattc ttcactgggt tcttctgaga ttgaacctac 2640

aggtgtttgc caagtgcctg gcccagagca agtggccact gcttctccca tctctctcct 2700

gcccaacctg gtagagctga gggcatgaga ggcagagtgc acagtggtca agggtgcagc 2760

tctgcagcac aggcagccta ggcctgcgtc ccaacctgcc tctcaccagc tctgtgacct 2820

tgggcaaggg atttatctgt ctgtccctta gttttctcac ctgtaaaagg aggataagta 2880

tatatatata tttcccagtg ttgtgaagat taaaggagtt tatcgatgta ggtcttagga 2940

tgagtcctgg catttaccaa gggttggata tatgttatta tcactattaa gtgttgaggg 3000

tccaggcatg ctgggcaaca gggaccccat ctctacaaaa aagtttaaaa aattagccag 3060

gcgtggtggt gcacctgtcg tcttagctac ttgggaggct gaggtgggag gatcacttga 3120

gcccagaagc ttgaagctgc agtgagctag gatcgtgcca ctgcactcca acctgggtga 3180

gagagcgaga ccctgtctca agaaaaagaa aaatgcagag aaacaggagt cttggctact 3240

cctttagagg cagactcaga ccctcctgcc tcacagcttt atctttgtat ttgcccctta 3300

ctttatcttg tgccttgaga aattgctggg gagagaggta tgtccactgg gcagctgtac 3360

aggatggagg atatagggcg tttccactcc cagcagccag gttccctcac cccaagctca 3420

cccactgttg gggagattat ctacaataac accagaaaca cattggggtg gattgggggt 3480

atccttatgg gttcttttca gggaaccatt gctggacaag gcacaggagc cacctccatt 3540

tctgagctct gcaagggaca agaactagag ccatcagggg ctgggctcac tgtggcccca 3600

ccccaagccg tcagcctcca gggatctaca ccctgccttg gctgctacag ctttttcact 3660

ccactgccct aggggagttc agcaacctaa tgatctctat ctctgaacat ctcttcatcc 3720

catgctccaa gtccagcaac ctgcaccctg gaaccaggag tggaccctac ccgagctgtc 3780

tgtattaatc cccatccccc accaccaatc ttaaaaagcc ctctgtcccc ctaccctaaa 3840

ccccagttag gtacccatgc tgggcaggtc agttaacaat ttatgcacag gtactagttt 3900

tattgtatta ccgttccagg gtagctttga aaaaagtatc tcaaaaaggc aacatgggcc 3960

gagcgcagtg gctcacgcct gtaatcccag cactttggga ggccaaggtg ggcagatcgc 4020

ctgaggtctg gagttcaaga ccagcctggc caacagggtg aaaccccgtc tctacaaaaa 4080

taagaaaatt agccaggtgt agtggcagac gtctgtaatc ccagctattc aggaggctga 4140

ggcacgagaa ttccatgaac ccaggatgcg gaggttgcag tgagccgaga ttgtgccact 4200

gcgctccagc ctgggcgaca gagtggtatt ctgtttc 4237

<210> 6

<211> 540

<212> PRT

<213> Homo sapiens

<400> 6

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe
1 5 10 15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
20 25 30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
35 40 45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
50 55 60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu
65 70 75 80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser Tyr Gln
85 90 95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu
100 105 110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
115 120 125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
130 135 140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145 150 155 160

```
Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly
                165                 170                 175

Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser
            180                 185                 190

Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His Thr Ala
        195                 200                 205

Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser
    210                 215                 220

Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu
225                 230                 235                 240

Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser
                245                 250                 255

Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly
            260                 265                 270

Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu
        275                 280                 285

Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro
    290                 295                 300

Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser
305                 310                 315                 320

Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val
                325                 330                 335

Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn
            340                 345                 350

Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val
        355                 360                 365

Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg
    370                 375                 380

Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly
385                 390                 395                 400

Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser
                405                 410                 415
```

Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe
420 425 430

Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly
435 440 445

Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly
450 455 460

Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu
465 470 475 480

Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln
485 490 495

Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser
500 505 510

Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val
515 520 525

Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
530 535 540

<210> 7

<211> 508

<212> PRT

<213> artificial sequence

<220>

<223> fragment

<400> 7

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe
1 5 10 15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
20 25 30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
35 40 45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
50 55 60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu
65 70 75 80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Glu Ser Tyr Gln
85 90 95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu
100 105 110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
115 120 125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
130 135 140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145 150 155 160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly
165 170 175

Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser
180 185 190

Ser Gly His Gln Glu Lys Asp Thr Glu Leu Gly Ser Thr His Thr Ala
195 200 205

Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser
210 215 220

Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu
225 230 235 240

Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser
245 250 255

Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly
260 265 270

Ala Glu Ser Asp Gln Ala Pro Ile Ile Cys Ser Ser Gly Ala Glu Ala
275 280 285

Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro Val
290 295 300

Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser Thr

305 310 315 320

Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val Pro
325 330 335

Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn Ser Thr
340 345 350

Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val Leu Thr
355 360 365

Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg Asn Glu
370 375 380

Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly Ser Ser
385 390 395 400

Ala Trp Leu Asp Ser Ser Phe Glu Asn Arg Gly Leu Gly Ser Glu Leu
405 410 415

Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe Ser Gly
420 425 430

Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly Met Gly
435 440 445

Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly Thr Phe
450 455 460

Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu Gly Asn
465 470 475 480

Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln Ala Asp
485 490 495

Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg
500 505

<210> 8

<211> 239

<212> PRT

<213> artificial sequence

<220>

<223> Fragment

<400> 8

```
Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe
1               5                  10                  15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
            20                  25                  30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
        35                  40                  45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
    50                  55                  60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu
65                  70                  75                  80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Glu Ser Tyr Gln
                85                  90                  95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu
            100                 105                 110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
        115                 120                 125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
    130                 135                 140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145                 150                 155                 160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly
                165                 170                 175

Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser
            180                 185                 190

Ser Gly His Gln Glu Lys Asp Thr Glu Leu Gly Ser Thr His Thr Ala
        195                 200                 205

Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser
    210                 215                 220

Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg
225                 230                 235
```

<210> 9

<211> 236

<212> PRT

<213> artificial sequence

<220>

<223> Fragment

<400> 9

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe
1 5 10 15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
20 25 30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
35 40 45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
50 55 60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu
65 70 75 80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Glu Ser Tyr Gln
85 90 95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu
100 105 110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
115 120 125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
130 135 140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145 150 155 160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly
165 170 175

Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser
180 185 190

Ser Gly His Gln Glu Lys Asp Thr Glu Leu Gly Ser Thr His Thr Ala
195 200 205

Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser
210 215 220

Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg
225 230 235

<210> 10

<211> 232

<212> PRT

<213> artificial sequence

<220>

<223> Fragment

<400> 10

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe
1 5 10 15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
20 25 30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
35 40 45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
50 55 60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu
65 70 75 80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Glu Ser Tyr Gln
85 90 95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu
100 105 110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
115 120 125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val

130 135 140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145 150 155 160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly
165 170 175

Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser
180 185 190

Ser Gly His Gln Glu Lys Asp Thr Glu Leu Gly Ser Thr His Thr Ala
195 200 205

Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser
210 215 220

Val Ser Phe Gln Pro Leu Ala Arg
225 230

<210> 11

<211> 171

<212> PRT

<213> artificial sequence

<220>

<223> Fragment

<400> 11

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe
1 5 10 15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
20 25 30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
35 40 45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
50 55 60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu
65 70 75 80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Glu Ser Tyr Gln
85 90 95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu
100 105 110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
115 120 125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
130 135 140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145 150 155 160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg
165 170

<210> 12

<211> 167

<212> PRT

<213> artificial sequence

<220>

<223> Fragment

<400> 12

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe
1 5 10 15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
20 25 30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
35 40 45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
50 55 60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu
65 70 75 80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Glu Ser Tyr Gln
85 90 95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu
100 105 110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
115 120 125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
130 135 140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145 150 155 160

Leu Gln Thr Leu Ser Pro Arg
165

<210> 13

<211> 341

<212> PRT

<213> artificial sequence

<220>

<223> Fragment

<400> 13

Ala Ile Pro Arg Asn Pro Asp Gly Gly Pro Leu Glu Ser Ser Ser Asp
1 5 10 15

Leu Ala Ala Leu Ser Pro Leu Thr Ser Ser Gly His Gln Glu Lys Asp
20 25 30

Thr Glu Leu Gly Ser Thr His Thr Ala Gly Ala Thr Ser Ser Leu Thr
35 40 45

Pro Ser Arg Gly Pro Val Ser Pro Ser Val Ser Phe Gln Pro Leu Ala
50 55 60

Arg Ser Thr Pro Arg Ala Ser Arg Leu Pro Gly Pro Thr Gly Ser Val
65 70 75 80

Val Ser Thr Gly Thr Ser Phe Ser Ser Ser Ser Pro Gly Leu Ala Ser
85 90 95

Ala Gly Ala Ala Glu Gly Lys Gln Gly Ala Glu Ser Asp Gln Ala Pro
100 105 110

Ile Ile Cys Ser Ser Gly Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser
115 120 125

Lys Val Pro Thr Thr Leu Met Pro Val Asn Thr Val Ala Leu Lys Val
130 135 140

Pro Ala Asn Pro Ala Ser Val Ser Thr Val Pro Ser Lys Leu Pro Thr
145 150 155 160

Ser Ser Lys Pro Pro Gly Ala Val Pro Asn Ala Leu Thr Asn Pro Ala
165 170 175

Pro Ser Lys Leu Pro Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser
180 185 190

Lys Val Pro Thr Ser Met Val Leu Thr Lys Val Ser Ala Ser Thr Val
195 200 205

Pro Thr Asp Gly Ser Ser Arg Asn Glu Glu Thr Pro Ala Ala Pro Thr
210 215 220

Pro Ala Gly Ala Thr Gly Gly Ser Ser Ala Trp Leu Asp Ser Ser Phe
225 230 235 240

Glu Asn Arg Gly Leu Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala
245 250 255

Ser Gln Val Asp Ser Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile
260 265 270

Ser Ala Ser Thr Ser Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu
275 280 285

Asn Glu Tyr Lys Ser Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn
290 295 300

Pro Ser Ile Gln Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro
305 310 315 320

Asp Gly Gly Pro Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu
325 330 335

Val Pro Cys His Arg
340

<210> 14

<211> 337

<212> PRT

<213> artificial sequence

<220>

<223> Fragment

<400> 14

Asn Pro Asp Gly Gly Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu
1 5 10 15

Ser Pro Leu Thr Ser Ser Gly His Gln Glu Lys Asp Thr Glu Leu Gly
20 25 30

Ser Thr His Thr Ala Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly
35 40 45

Pro Val Ser Pro Ser Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro
50 55 60

Arg Ala Ser Arg Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly
65 70 75 80

Thr Ser Phe Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala
85 90 95

Glu Gly Lys Gln Gly Ala Glu Ser Asp Gln Ala Pro Ile Ile Cys Ser
100 105 110

Ser Gly Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr
115 120 125

Thr Leu Met Pro Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro
130 135 140

Ala Ser Val Ser Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro
145 150 155 160

Pro Gly Ala Val Pro Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu
165 170 175

Pro Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr
180 185 190

Ser Met Val Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly
195 200 205

Ser Ser Arg Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala
210 215 220

Thr Gly Gly Ser Ser Ala Trp Leu Asp Ser Ser Phe Glu Asn Arg Gly
225 230 235 240

Leu Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp
245 250 255

Ser Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr
260 265 270

Ser Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys
275 280 285

Ser Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln
290 295 300

Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro
305 310 315 320

Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His
325 330 335

Arg

<210> 15

<211> 276

<212> PRT

<213> artificial sequence

<220>

<223> Fragment

<400> 15

Ser Thr Pro Arg Ala Ser Arg Leu Pro Gly Pro Thr Gly Ser Val Val
1 5 10 15

Ser Thr Gly Thr Ser Phe Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala
20 25 30

Gly Ala Ala Glu Gly Lys Gln Gly Ala Glu Ser Asp Gln Ala Pro Ile
35 40 45

Ile Cys Ser Ser Gly Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser Lys
50 55 60

Val Pro Thr Thr Leu Met Pro Val Asn Thr Val Ala Leu Lys Val Pro
65 70 75 80

Ala Asn Pro Ala Ser Val Ser Thr Val Pro Ser Lys Leu Pro Thr Ser
85 90 95

Ser Lys Pro Pro Gly Ala Val Pro Asn Ala Leu Thr Asn Pro Ala Pro
100 105 110

Ser Lys Leu Pro Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser Lys
115 120 125

Val Pro Thr Ser Met Val Leu Thr Lys Val Ser Ala Ser Thr Val Pro
130 135 140

Thr Asp Gly Ser Ser Arg Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro
145 150 155 160

Ala Gly Ala Thr Gly Gly Ser Ser Ala Trp Leu Asp Ser Ser Phe Glu
165 170 175

Asn Arg Gly Leu Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser
180 185 190

Gln Val Asp Ser Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser
195 200 205

Ala Ser Thr Ser Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn
210 215 220

Glu Tyr Lys Ser Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn Pro
225 230 235 240

Ser Ile Gln Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp
245 250 255

Gly Gly Pro Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val
260 265 270

Pro Cys His Arg

275

<210> 16

<211> 272

<212> PRT

<213> artificial sequence

<220>

<223> Fragment

<400> 16

Ala Ser Arg Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr
1 5 10 15

Ser Phe Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu
20 25 30

Gly Lys Gln Gly Ala Glu Ser Asp Gln Ala Pro Ile Ile Cys Ser Ser
35 40 45

Gly Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr
50 55 60

Leu Met Pro Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala
65 70 75 80

Ser Val Ser Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro
85 90 95

Gly Ala Val Pro Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro
100 105 110

Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser
115 120 125

Met Val Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser
130 135 140

Ser Arg Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr
145 150 155 160

Gly Gly Ser Ser Ala Trp Leu Asp Ser Ser Phe Glu Asn Arg Gly Leu
165 170 175

Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser
180 185 190

Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser
195 200 205

Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser
210 215 220

Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu
225 230 235 240

Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg
245 250 255

Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg
260 265 270

<210> 17

<211> 269

<212> PRT

<213> Artificial Sequence

<220>

<223> Fragment

<400> 17

Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser
1 5 10 15

Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln
20 25 30

Gly Ala Glu Ser Asp Gln Ala Pro Ile Ile Cys Ser Ser Gly Ala Glu
35 40 45

Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro
50 55 60

Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser
65 70 75 80

Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val
85 90 95

Pro Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn Ser
100 105 110

Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val Leu
115 120 125

Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg Asn
130 135 140

Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly Ser
145 150 155 160

Ser Ala Trp Leu Asp Ser Ser Phe Glu Asn Arg Gly Leu Gly Ser Glu
165 170 175

Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe Ser
180 185 190

Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly Met
195 200 205

Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly Thr
210 215 220

Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu Gly
225 230 235 240

Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln Ala
245 250 255

Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg
260 265

<210> 18

<211> 510

<212> PRT

<213> Artificial Sequence

<220>

<223> Fragment

<400> 18

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe
1 5 10 15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
20 25 30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
35 40 45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
50 55 60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu
65 70 75 80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Glu Ser Tyr Gln
85 90 95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu
100 105 110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
115 120 125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
130 135 140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145 150 155 160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly
165 170 175

Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser
180 185 190

Ser Gly His Gln Glu Lys Asp Thr Glu Leu Gly Ser Thr His Thr Ala
195 200 205

Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser
210 215 220

Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu
225 230 235 240

Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser
245 250 255

Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly

260 265 270

Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu
275 280 285

Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro
290 295 300

Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser
305 310 315 320

Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val
325 330 335

Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn
340 345 350

Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val
355 360 365

Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg
370 375 380

Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly
385 390 395 400

Ser Ser Ala Trp Leu Asp Ser Ser Phe Glu Asn Arg Gly Leu Gly Ser
405 410 415

Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe
420 425 430

Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly
435 440 445

Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly
450 455 460

Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu
465 470 475 480

Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln
485 490 495

Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg
500 505 510

<210> 19

<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> Primer Rantes sense

<400> 19
cgctgtcatc ctcattgcta 20

<210> 20

<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> Primer Rantes antisense

<400> 20
gcacttgcca ctggtgtaga 20

<210> 21

<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> Primer IL-8 sense

<400> 21
ctgcgccaac acagaaatta 20

<210> 22

<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> Primer IL-8 antisense

<400> 22
tgaattctca gccctcttca 20

<210> 23

<211> 21

<212> PRT

<213> artificial sequence

<220>

<223> Peptide for immunization

<400> 23

Pro Met Pro Val Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn
1 5 10 15

Ser Glu Gln Ala Leu
20

<210> 24

<211> 15

<212> PRT

<213> artificial sequence

<220>

<223> Peptide for immunozation

<400> 24

Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln Ala Asp Arg Lys
1 5 10 15

<210> 25

<211> 12

<212> PRT

<213> artificial sequence

<220>

<223> Peptide for immunozation

<400> 25

Ser Lys Leu Pro Ile Asn Ser Thr Arg Ala Gly Met
1 5 10

<210> 26

<211> 7

<212> PRT

<213> artificial sequence

<220>

<223> peptide pWobble

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> Xaa = Leu or Val

<400> 26

Xaa Pro Ser Lys Xaa Pro Thr
1 5

<210> 27

<211> 7

<212> PRT

<213> artificial sequence

<220>

<223> Peptide p3061

<400> 27

Leu Pro Ser Lys Leu Pro Thr
1 5

<210> 28

<211> 7

<212> PRT

<213> artificial sequence

<220>

<223> SEP fragment I

<400> 28

Leu Pro Ser Lys Leu Pro Thr
1 5

<210> 29

<211> 7

<212> PRT

<213> artificial sequence

<220>

<223> SEP fragment II

<400> 29

Leu Pro Ser Lys Val Pro Thr
1 5

<210> 30

<211> 7

<212> PRT

<213> artificial sequence

<220>

<223> SEP fragment III

<400> 30

Val Pro Ser Lys Leu Pro Thr
1 5

<210> 31

<211> 7

<212> PRT

<213> artificial sequence

<220>

<223> SEP fragment IV

<400> 31

Val Pro Ser Lys Val Pro Thr
1 5